assigned ATCC deposit no.209722.

Analysis of the amino acid sequence of the full-length PRO705 polypeptide suggests that it possesses significant sequence similarity to the K-glypican protein, thereby indicating that PRO705 may be a novel glypican protein family member. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO705 amino acid sequence and the following Dayhoff sequences, GPCK_MOUSE, GLYP_CHICK, GLYP_RAT, GLYP_HUMAN, GPC2_RAT, GPC5_HUMAN, GPC3_HUMAN, GPC3_RAT, P_R30168 and CEC03H12_2.

EXAMPLE 19: Isolation of cDNA Clones Encoding Human PRO708

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA34024. Based on the DNA34024 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO708.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCCAACCCAACTGTTTACCTCTGG-3' (SEQ ID NO:115)

reverse PCR primer 5'-CTCTCTGAGTGTACATCTGTGTGG-3' (SEQ ID NO:116)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA34024 sequence which had the following nucleotide sequence

hybridization probe

5'-GCCACCCTACCTCAGAAACTGAAGGAGGTTGGNTATTCAACGCATATGGTCGG-3' (SEQ ID NO:117)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO708 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO708 [herein designated as UNQ372 (DNA48296-1292)] (SEQ ID NO:113) and the derived protein sequence for PRO708.

The entire nucleotide sequence of UNQ372 (DNA48296-1292) is shown in Figures 42A-B (SEQ ID NO:113). Clone UNQ372 (DNA48296-1292) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 891-893 and ending at the stop codon at nucleotide positions 2436-2438 (Figures 42A-B). The predicted polypeptide precursor is 515 amino acids long (Figure 43). The full-length PRO708 protein shown in Figure 43 has an estimated molecular weight of about 56,885 daltons and a pI of about 6.49. Analysis of the PRO708 amino acid sequence shown in Figure 43 (SEQ ID NO:114) evidences the existence of a putative signal peptide at about amino acid 1 to about amino acid 37, putative sulfatase signature sequences at about amino acid 120 to about amino acid 132 and about amino acid 168 to about amino acid 177, a putative tyrosine kinase phosphorylation site from about amino acid 163 to about amino acid 169 and potential N-glycosylation sites from about amino acid 157 to about amino acid 160, about amino acid 306 to about amino

acid 309 and about amino acid 318 to about amino acid 321. Clone UNQ372 (DNA48296-1292) has been deposited with ATCC on March 11, 1998 and is assigned ATCC deposit no. 209668.

Analysis of the amino acid sequence of the full-length PRO708 polypeptide suggests that it possesses significant homology to the aryl sulfatase proteins, thereby indicating that PRO708 may be a novel aryl sulfatase homolog. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO708 amino acid sequence and the following Dayhoff sequences, ARSB_HUMAN, CELC54D2_2, G02857, STS_HUMAN, I37186, I37187, GEN12648, CELD1014_7, GA6S_HUMAN and SPHM_HUMAN.

EXAMPLE 20: Isolation of cDNA Clones Encoding Human PRO320

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA28739. Based on the DNA28739 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO320.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCTCAGTGGCCACATGCTCATG-3' (SEQ ID NO:120)

reverse PCR primer 5'-GGCTGCACGTATGGCTATCCATAG-3' (SEQ ID NO:121)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28739 sequence which had the following nucleotide sequence

hybridization probe

5'-GATAAACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCC-3' (SEQ ID NO:122)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO320 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB25).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO320 [herein designated as UNQ281 (DNA32284-1307)] (SEQ ID NO:118) and the derived protein sequence for PRO320.

The entire nucleotide sequence of UNQ281 (DNA32284-1307) is shown in Figure 44 (SEQ ID NO:118). Clone UNQ281 (DNA32284-1307) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 135-137 and ending at the stop codon at nucleotide positions 1149-1151 (Figure 44). The predicted polypeptide precursor is 338 amino acids long (Figure 45). The full-length PRO320 protein shown in Figure 45 has an estimated molecular weight of about 37,143 daltons and a pI of about 8.92. Important regions of the PRO320 amino acid sequence include the signal peptide, corresponding to amino acids 1-21, an EGF-like domain cysteine pattern signature, corresponding to amino acids 80-91, and three calcium-binding EGF-like domains, corresponding to amino acids 103-124, 230-151 and 185-206, respectively. Clone UNQ281 (DNA32284-1307) has been deposited with ATCC and is assigned ATCC deposit no. 209670.

EXAMPLE 21: Isolation of cDNA Clones Encoding Human PRO324

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA34347. Based on the DNA34347 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO324.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GCAATGAACTGGGAGCTGC-3' (SEQ ID NO:125)

forward PCR primer 2 5'-CTGTGAATAGCATCCTGGG-3' (SEQ ID NO:126)

forward PCR primer 3 5'-CTTTTCAAGCCACTGGAGGG-3' (SEQ ID NO:127)

reverse PCR primer 1 5'-CTGTAGACATCCAAGCTGGTATCC-3' (SEQ ID NO:128)

reverse PCR primer 2 5'-AAGAGTCTGCATCCACACCACTC-3' (SEQ ID NO:129)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA34347 sequence which had the following nucleotide sequence

hybridization probe

5'-ACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCCAGAATG-3' (SEQ ID NO:130)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with one of the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO324 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB6).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO324 [herein designated as UNQ285 (DNA36343-1310)] (SEQ ID NO:123) and the derived protein sequence for PRO324.

The entire nucleotide sequence of UNQ285 (DNA36343-1310) is shown in Figure 46 (SEQ ID NO:123). Clone UNQ285 (DNA36343-1310) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 144-146 and ending at the stop codon at nucleotide positions 1011-1013 (Figure 46). The predicted polypeptide precursor is 289 amino acids long (Figure 47). The full-length PRO324 protein shown in Figure 47 has an estimated molecular weight of about 32,268 daltons and a pI of about 9.21. Analysis of the PRO324 polypeptide sequence shown in Figure 47 (SEQ ID NO:124) evidence the presence of the following: a signal peptide from about amino acid 1 to about amino acid 31, a transmembrane domain from about amino acid 136 to about amino acid 157, tyrosine kinase phosphorylation sites from about amino acid 106 or about amino acid 107 to about amino acid 113 and regions that are homologous to short-chain alcohol dehydrogenase regions from about amino acid 80 to about amino acid 90, from about amino acid 131 to about amino acid 168, from about amino acid 1 to about amino acid 13 and from about amino acid 176 to about amino acid 185. Clone UNQ285 (DNA36343-1310) has been deposited with ATCC on March 30, 1998 and is assigned ATCC deposit no. 209718.

Analysis of the amino acid sequence of the full-length PRO324 polypeptide suggests that it possesses significant sequence similarity to oxidoreductases, thereby indicating that PRO324 may be a novel oxidoreductase